

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/589,870C  
Source: IFW/6  
Date Processed by STIC: 3-29-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 03/29/2005

PATENT APPLICATION: US/09/589,870C

TIME: 11:38:08

Input Set : D:\547.app.txt

Output Set: N:\CRF4\03292005\I589870C.raw

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4 <110> APPLICANT: Goshorn, Stephen C.
5     Graves, Scott Stoll
6     Schultz, Joanne Elaine
7     Lin, Yukang
8     Sanderson, James A.
9     Reno, John M.
11 <120> TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
12     METHODS OF USE THEREOF
15 <130> FILE REFERENCE: 110186.547
17 <140> CURRENT APPLICATION NUMBER: US 09/589,870C
18 <141> CURRENT FILING DATE: 2000-06-05
20 <150> PRIOR APPLICATION NUMBER: US 60/168,976
21 <151> PRIOR FILING DATE: 1999-12-03
23 <150> PRIOR APPLICATION NUMBER: US 60/137,900
24 <151> PRIOR FILING DATE: 1999-06-07
26 <160> NUMBER OF SEQ ID NOS: 48
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 638
32 <212> TYPE: DNA
33 <213> ORGANISM: Streptomyces avidinii
35 <400> SEQUENCE: 1
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37 cgtcggttgca gccatcgccg tttccctgac caccggtctcg attacggcca gcgcttcggc      120
38 agaccctcc aaggactcga aggccagggt ctcggccgcc gaggccggca tcaccggcac      180
39 ctggtacaac cagctcggct cgaccttcac cgtgaccgcg ggcgccgacg gcgcctgac      240
40 cggaacctac gagtcggccg tcggcaacgc cgagagccgc tacgtcctga ccggtcgta      300
41 cgacacgcgc ccggccaccg acggcagcgg caccgccctc ggttggacgg tggcctggaa      360
42 gaataactac cgcaacgccc actccgcgac cacgtggagc ggccagtagc tcggcggcgc      420
43 cgaggcgagg atcaacaccc agtggctgct gacctccggc accaccgagg ccaacgcctg      480
44 gaagtccacg ctggtcggcc acgacacctt caccaagggtg aagccgtccg ccgcctccat      540
45 cgacgcggcg aagaaggccg gcgtcaacaa cggaacccg ctcgacgcgc ttcagcagta      600
46 gtcgcgtccc ggcaccggcg ggtgccggga cctcggcc      638
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 183
50 <212> TYPE: PRT
51 <213> ORGANISM: Streptomyces avidinii
53 <400> SEQUENCE: 2
54 Met Arg Lys Ile Val Val Ala Ala Ile Ala Val Ser Leu Thr Thr Val
55 1           5           10           15
56 Ser Ile Thr Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala
57           20           25           30
58 Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln

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59          35          40          45
60 Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr
61          50          55          60
62 Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu
63 65          70          75          80
64 Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala
65          85          90          95
66 Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser
67          100          105          110
68 Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile
69          115          120          125
70 Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp
71          130          135          140
72 Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser
73 145          150          155          160
74 Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly Val Asn Asn Gly Asn
75          165          170          175
76 Pro Leu Asp Ala Val Gln Gln
77          180
79 <210> SEQ ID NO: 3
80 <211> LENGTH: 1612
81 <212> TYPE: DNA
82 <213> ORGANISM: Streptomyces avidinii
84 <400> SEQUENCE: 3
85 gaattcacga agtaaccgac aggactcggc cattctttgg ccgaaattcc tttgcagaaa      60
86 atgttggtga gaaccctccg atggctagta cgatttacac cgaacatgtg cccttggtcaa      120
87 ccatcgaccc ggacctcgac catccagttc tgccgcaaaa gacacatgcc gcaactgctgt      180
88 ttgttcaccg acaccgtcag gtgcacggcc gaggtcacaa accttgacgg gcgggatacg      240
89 gacggcgcac gccacagcgc gccctccgtc cccgcggggc aacaactagg gagtattttt      300
90 cgtgtctcac atgcgcaaga tcgtcgttgc agccatcgcc gtttcctga ccacggtctc      360
91 gattacggcc atggctgaca tccagatgac tcagtctcca tcgtccttgt ctgcctctgt      420
92 gggagacaga gtcacgatca cttgtcgggc tagtcagggc attagaggta atttagactg      480
93 gtatcagcag aaacctggta agggaccgaa actcctaate tactccacat ccaatttaa      540
94 ttctggtgtc ccatcaaggt tcagtggcag tgggtctggg tcagattata ctctcaccat      600
95 cagcagcctt cagcctgaag atttcgcaac gtattactgt ctacagcgta atgcgtatcc      660
96 gtacacgttc ggacaaggga ccaagctgga gatcaagatc tctggtggcg gtggtcggg      720
97 cgggtggtgg tgggtggcg gaggtcgag ccaggttcag ctggtccagt ctggggcaga      780
98 ggtgaaaaag ccaggggcct cagtcaaggt gtcttgcaag gcttctggct tcaacattaa      840
99 agacacctat atgcactggg tgaggcaggc acctggacag ggcctgcagt ggatgggaag      900
100 gattgatcct gcgaatggta atactaaatc cgacctgtcc ttccagggca gggtgactat      960
101 aacagcagac acgtccatca acacagccta catggaactc agcagcctga ggtctgacga      1020
102 cactgccgtc tattactggt ctagagaggt cctaactggg acgtggtctt tggactactg      1080
103 gggtaagga accttagtca ccgtgagctc tggctctggt tcggcagacc cctccaagga      1140
104 ctgaaggcc caggtctcgg ccgccgaggc cggcatcacc ggcacctggt acaaccagct      1200
105 cggtcgacc ttcacgtga ccgcgggcgc cgacggcgcc ctgaccggaa cctacgagtc      1260
106 ggccgtcggc aacgccgaga gccgctacgt cctgaccggt cgttacgaca gcgccccggc      1320
107 caccgacggc agcggcaccg ccctcggttg gacggtggcc tggagaata actaccgcaa      1380
108 cgccactcc gcgaccagct ggagcggcca gtacgtcggc ggcggcgagg cgaggatcaa      1440
109 caccagtggt ctgctgacct ccggcaccac cgaggccaac gcctggaagt ccacgtggt      1500

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110 cggccacgac accttcacca aggtgaagcc gtccgcccgc tccatcgacg cggcgaagaa      1560
111 ggccggcgtc aacaacggca acccgctcga cgccgttcag cagtaaggat cc      1612
113 <210> SEQ ID NO: 4
114 <211> LENGTH: 431
115 <212> TYPE: PRT
116 <213> ORGANISM: Streptomyces avidinii
118 <400> SEQUENCE: 4
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120 1 5 10 15
121 Ser Ile Thr Ala Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
122 20 25 30
123 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
124 35 40 45
125 Gln Gly Ile Arg Gly Asn Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys
126 50 55 60
127 Gly Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val
128 65 70 75 80
129 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr
130 85 90 95
131 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
132 100 105 110
133 Arg Asn Ala Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
134 115 120 125
135 Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
136 130 135 140
137 Gly Ser Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
138 145 150 155 160
139 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile
140 165 170 175
141 Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
142 180 185 190
143 Gln Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Ser Asp
144 195 200 205
145 Leu Ser Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ile Asn
146 210 215 220
147 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
148 225 230 235 240
149 Tyr Tyr Cys Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr
150 245 250 255
151 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Ser Ala
152 260 265 270
153 Asp Pro Ser Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly
154 275 280 285
155 Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr
156 290 295 300
157 Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly
158 305 310 315 320
159 Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro
160 325 330 335

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161 Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys
162           340           345           350
163 Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr
164           355           360           365
165 Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser
166           370           375           380
167 Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp
168 385           390           395           400
169 Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys
170           405           410           415
171 Lys Ala Gly Val Asn Asn Gly Asn Pro Leu Asp Ala Val Gln Gln
172           420           425           430
174 <210> SEQ ID NO: 5
175 <211> LENGTH: 1239
176 <212> TYPE: DNA
177 <213> ORGANISM: Streptomyces avidinii
179 <400> SEQUENCE: 5
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181 atgacttgca gggccagctc aagtgttaagt tacatgcact ggtaccagca gaagccagga      120
182 tcctccccc aacctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc      180
183 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa      240
184 gatgctgcc cttattactg ccagcagtg attagtaacc caccacggt cgggtgctggg      300
185 accaagctgg agctgaagat ctctggtctg gaaggcagcc cggaagcagg tctgtctccg      360
186 gacgcaggtt ccggctcgag ccaggttcag ctggtccagt caggggctga gctggtgaag      420
187 cctggggcct cagtgaagat gtcttgcaag gcttctggct acacatttac cagttacaat      480
188 atgcactggg taaagcagac acctggacag ggctggaat ggattggagc tatttatcca      540
189 ggaaatggtg atacttcta caatcagaag ttcaaaggca aggccacatt gactgcagac      600
190 aaatcctcca gcacagccta catgcagctc agcagcctga catctgagga ctctgcggtc      660
191 tattactgtg caagagcgca attacgacct aactactggt acttcgatgt ctggggcgca      720
192 gggaccacgg tcaccgtgag ctctggtctt ggttcggcag acccctccaa ggactcgaag      780
193 gcccaggtct cggccgcccga ggccggcatc accggcacct ggtacaacca gctcggctcg      840
194 accttcacg tgaccgcggg cgccgacggc gccctgaccg gaacctacga gtcggcgctc      900
195 ggcaacgccc agagccgcta cgtcctgacc ggtcgttacg acagcgccc ggccaccgac      960
196 ggcagcgcca ccgcccctcg ttggacgggt gcttgggaaga ataactaccg caacgcccac      1020
197 tccgcgacca cgtggagcgg ccagtacgtc ggcgggcgcc aggcgaggat caacacccag      1080
198 tggtgctga cctccggcac caccgagggc aacgcctgga agtccacgct ggtcggccac      1140
199 gacaccttca ccaaggtgaa gccgtccgcc gccctcatcg acgcggcgaa gaaggccggc      1200
200 gtcaacaacg gcaacccgct cgacgccgtt cagcagtaa      1239
202 <210> SEQ ID NO: 6
203 <211> LENGTH: 412
204 <212> TYPE: PRT
205 <213> ORGANISM: Streptomyces avidinii
207 <400> SEQUENCE: 6
208 Asp Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
209 1           5           10           15
210 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
211           20           25           30
212 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
213           35           40           45

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214 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
215      50                      55                      60
216 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
217 65                      70                      75                      80
218 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
219                      85                      90                      95
220 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Ile Ser Gly Leu Glu Gly
221                      100                      105                      110
222 Ser Pro Glu Ala Gly Leu Ser Pro Asp Ala Gly Ser Gly Ser Ser Gln
223                      115                      120                      125
224 Val Gln Leu Val Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
225      130                      135                      140
226 Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn
227 145                      150                      155                      160
228 Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly
229                      165                      170                      175
230 Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys
231                      180                      185                      190
232 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
233                      195                      200                      205
234 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
235      210                      215                      220
236 Arg Ala Gln Leu Arg Pro Asn Tyr Trp Tyr Phe Asp Val Trp Gly Ala
237 225                      230                      235                      240
238 Gly Thr Thr Val Thr Val Ser Ser Gly Ser Gly Ser Ala Asp Pro Ser
239                      245                      250                      255
240 Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly
241                      260                      265                      270
242 Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala
243      275                      280                      285
244 Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu
245      290                      295                      300
246 Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp
247 305                      310                      315                      320
248 Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr
249                      325                      330                      335
250 Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly
251                      340                      345                      350
252 Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr
253                      355                      360                      365
254 Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr
255      370                      375                      380
256 Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly
257 385                      390                      395                      400
258 Val Asn Asn Gly Asn Pro Leu Asp Ala Val Gln Gln
259                      405                      410
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262 <211> LENGTH: 1280
263 <212> TYPE: DNA

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**VERIFICATION SUMMARY**

DATE: 03/29/2005

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Input Set : D:\547.app.txt

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